

SEQUENCE LISTING

<110> EXONHIT THERAPEUTICS SA

<120> Compositions a,d methods to inhibit the production of Abeta peptide

<130> B0229WO

<150> US 60/517,401

<151> 2003-11-06

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 1368

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1368)

<223>

<400> 1	
atg gcc caa gcc ctg ccc tgg ctc ctg ctg tgg atg ggc gcg gga gtg	48
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val	
1 5 10 15	
ctg cct gcc cac ggc acc cag cac ggc atc cgg ctg ccc ctg cgc agc	96
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser	
20 25 30	
ggc ctg ggg ggc gcc ccc ctg ggg ctg cgg ctg ccc cgg gag acc gac	144
Gly Leu Gly Gly Ala Pro Leu Gly Gly Leu Arg Leu Pro Arg Glu Thr Asp	
35 40 45	
gaa gag ccc gag gag ccc ggc cgg agg ggc agc ttt gtg gag atg gtg	192
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val	
50 55 60	

gac Asp 65	aac Asn	ctg Leu	agg Arg	ggc Gly	aag Lys 70	tcg Ser	ggg Gly	cag Gln	ggc Gly	tac Tyr 75	tac Tyr	gtg Val	gag Glu	atg Met	acc Thr 80	240
gtg Val	ggc Gly	agc Ser	ccc Pro	ccg Pro 85	cag Gln	acg Thr	ctc Leu	aac Asn	atc Ile 90	ctg Leu	gtg Val	gat Asp	aca Thr	ggc Gly 95	agc Ser	288
agt Ser	aac Asn	ttt Phe	gca Ala 100	gtg Val	ggc Gly	gct Ala	gcc Ala	ccc Pro 105	cac His	ccc Pro	ttc Phe	ctg Leu	cat His 110	cgc Arg	tac Tyr	336
tac Tyr	cag Gln	agg Arg 115	cag Gln	ctg Leu	tcc Ser	agc Ser	aca Thr 120	tac Tyr	cgg Arg	gac Asp	ctc Leu	cgg Arg 125	aag Lys	ggc Gly	gtg Val	384
tat Tyr	gtg Val 130	ccc Pro	tac Tyr	acc Thr	cag Gln	ggc Gly 135	aag Lys	tgg Trp	gaa Glu	ggg Gly	gag Glu 140	ctg Leu	ggc Gly	acc Thr	gac Asp	432
ctg Leu 145	gta Val	agc Ser	atc Ile	ccc Pro	cat His 150	ggc Gly	ccc Pro	aac Asn	gtc Val	act Thr 155	gtg Val	cgt Arg	gcc Ala	aac Asn	att Ile 160	480
gct Ala	gcc Ala	atc Ile	act Thr	gaa Glu 165	tca Ser	gac Asp	aag Lys	ttc Phe	ttc Phe 170	atc Ile	aac Asn	ggc Gly	tcc Ser	aac Asn 175	tgg Trp	528
gaa Glu	ggc Gly	atc Ile	ctg Leu 180	ggg Gly	ctg Leu	gcc Ala	tat Tyr	gct Ala 185	gag Glu	att Ile	gcc Ala	agg Arg	atc Ile 190	att Ile	gga Gly	576
ggc Gly	atc Ile	gac Asp 195	cac His	tcg Ser	ctg Leu	tac Tyr	aca Thr 200	ggc Gly	agt Ser	ctc Leu	tgg Trp	tat Tyr 205	aca Thr	ccc Pro	atc Ile	624
cgg Arg	cgg Arg 210	gag Glu	tgg Trp	tat Tyr	tat Tyr	gag Glu 215	gtc Val	atc Ile	att Ile	gtg Val	cgg Arg 220	gtg Val	gag Glu	atc Ile	aat Asn	672
gga Gly 225	cag Gln	gat Asp	ctg Leu	aaa Lys	atg Met 230	gac Asp	tgc Cys	aag Lys	gag Glu	tac Tyr 235	aac Asn	tat Tyr	gac Asp	aag Lys	agc Ser 240	720
att Ile	gtg Val	gac Asp	agt Ser	ggc Gly 245	acc Thr	acc Thr	aac Asn	ctt Leu	cgt Arg 250	ttg Leu	ccc Pro	aag Lys	aaa Lys	gtg Val 255	ttt Phe	768
gaa Glu	gct Ala	gca Ala	gtc Val 260	aaa Lys	tcc Ser	atc Ile	aag Lys	gca Ala 265	gcc Ala	tcc Ser	tcc Ser	acg Thr	gag Glu 270	aag Lys	ttc Phe	816
cct Pro	gat Asp	ggc Gly 275	ttc Phe	tgg Trp	cta Leu	gga Gly	gag Glu 280	cag Gln	ctg Leu	gtg Val	tgc Cys	tgg Trp 285	caa Gln	gca Ala	ggc Gly	864
acc Thr 290	acc Thr	cct Pro	tgg Trp	aac Asn	att Ile	ttc Phe 295	cca Pro	gtc Val	atc Ile	tca Ser	ctc Leu 300	tac Tyr	cta Leu	atg Met	ggc Gly	912
gag Glu 305	gtt Val	acc Thr	aac Asn	cag Gln	tcc Ser 310	ttc Phe	cgc Arg	atc Ile	acc Thr	atc Ile 315	ctt Leu	ccg Pro	cag Gln	caa Gln	tac Tyr 320	960
ctg Leu	cgg Arg	cca Pro	gtg Val	gaa Glu 325	gat Asp	gtg Val	gcc Ala	acg Thr	tcc Ser 330	caa Gln	gac Asp	gac Asp	tgt Cys	tac Tyr 335	aag Lys	1008

ttt ggc atc tca cag tca tcc acg ggc act gtt atg gga gct gtt atc	1056
Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile	
	340
atg gag ggc ttc tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc	1104
Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly	
	355
ttt gct gtc agc gct tgc cat gtg cac gat gag ttc agg acg gca gcg	1152
Phe Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala	
	370
gtg gaa ggc cct ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac	1200
Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn	
	385
att cca cag aca gat gag tca acc ctc atg acc ata gcc tat gtc atg	1248
Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met	
	405
gct gcc atc tgc gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt	1296
Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys	
	420
cag tgg cgc tgc ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct	1344
Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala	
	435
gat gac atc tcc ctg ctg aag tga	1368
Asp Asp Ile Ser Leu Leu Lys	
	450

<210> 2

<211> 455

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val	
1 5 10 15	
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser	
20 25 30	
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp	
35 40 45	
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val	
50 55 60	
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr	
65 70 75 80	
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser	

Ser	Asn	Phe	Ala 100	Val	Gly	Ala	Ala	Pro 105	His	Pro	Phe	Leu	His 110	Arg	Tyr
Tyr	Gln	Arg 115	Gln	Leu	Ser	Ser	Thr 120	Tyr	Arg	Asp	Leu	Arg 125	Lys	Gly	Val
Tyr	Val 130	Pro	Tyr	Thr	Gln	Gly 135	Lys	Trp	Glu	Gly	Glu 140	Leu	Gly	Thr	Asp
Leu 145	Val	Ser	Ile	Pro	His 150	Gly	Pro	Asn	Val	Thr 155	Val	Arg	Ala	Asn	Ile 160
Ala	Ala	Ile	Thr	Glu 165	Ser	Asp	Lys	Phe	Phe 170	Ile	Asn	Gly	Ser	Asn 175	Trp
Glu	Gly	Ile	Leu 180	Gly	Leu	Ala	Tyr	Ala 185	Glu	Ile	Ala	Arg	Ile 190	Ile	Gly
Gly	Ile	Asp 195	His	Ser	Leu	Tyr	Thr 200	Gly	Ser	Leu	Trp	Tyr 205	Thr	Pro	Ile
Arg	Arg 210	Glu	Trp	Tyr	Tyr	Glu 215	Val	Ile	Ile	Val	Arg 220	Val	Glu	Ile	Asn
Gly 225	Gln	Asp	Leu	Lys	Met 230	Asp	Cys	Lys	Glu	Tyr 235	Asn	Tyr	Asp	Lys	Ser 240
Ile	Val	Asp	Ser	Gly 245	Thr	Thr	Asn	Leu	Arg 250	Leu	Pro	Lys	Lys	Val 255	Phe
Glu	Ala	Ala	Val 260	Lys	Ser	Ile	Lys	Ala 265	Ala	Ser	Ser	Thr	Glu 270	Lys	Phe
Pro	Asp	Gly 275	Phe	Trp	Leu	Gly	Glu 280	Gln	Leu	Val	Cys	Trp 285	Gln	Ala	Gly
Thr	Thr 290	Pro	Trp	Asn	Ile	Phe 295	Pro	Val	Ile	Ser	Leu 300	Tyr	Leu	Met	Gly
Glu 305	Val	Thr	Asn	Gln	Ser 310	Phe	Arg	Ile	Thr	Ile 315	Leu	Pro	Gln	Gln	Tyr 320
Leu	Arg	Pro	Val	Glu 325	Asp	Val	Ala	Thr	Ser 330	Gln	Asp	Asp	Cys	Tyr 335	Lys
Phe	Ala	Ile	Ser 340	Gln	Ser	Ser	Thr	Gly 345	Thr	Val	Met	Gly	Ala 350	Val	Ile

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 355 360 365

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 370 375 380

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 385 390 395 400

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
 405 410 415

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
 420 425 430

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
 435 440 445

Asp Asp Ile Ser Leu Leu Lys
 450 455

<210> 3

<211> 6

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 3

Ile Ala Arg Ile Ile Gly
 1 5

<210> 4

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 4

Glu Ile Ala Arg Ile Ile Gly
 1 5

<210> 5

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 5

Glu Ile Ala Arg Ile Ile Gly Gly
1 5

<210> 6

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 6

Ala Glu Ile Ala Arg Ile Ile Gly
1 5

<210> 7

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 7

Ala Glu Ile Ala Arg Ile Ile Gly Gly
1 5

<210> 8

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 8

Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1 5 10

<210> 9

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 9

Tyr Ala Glu Ile Ala Arg Ile Ile Gly
1 5

<210> 10

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 10

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly
1 5 10

<210> 11

<211> 11

<212> PRT

<213> artificial sequence

<220>

<223> distinctive fragment

<400> 11

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1 5 10

<210> 12

<211> 18

<212> DNA

<213> artificial sequence

<220>

<223> Probe

<400> 12

attgccagga tcattgga

18

<210> 13

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 13

aggcatcctg

10

<210> 14

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 14

gggctggcct

10

<210> 15

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 15
atgctgagat

10

<210> 16

<211> 6

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 16
tgccag

6

<210> 17

<211> 6

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 17
gatcat

6

<210> 18

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 18
tggaggtatc

10

<210> 19

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 19
gaccactcgc

10

<210> 20

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 20
tgtacacagg

10

<210> 21

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 21
cagtctctgg

10

<210> 22

<211> 6

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 22
caggat 6

<210> 23

<211> 8

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 23
ccaggatc 8

<210> 24

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 24
gccaggatca 10

<210> 25

<211> 18

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 25
attgccagga tcattgga 18

<210> 26

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 26

tgactgggaa caccccataa c

21

<210> 27

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 27

agttgtgcat gggagcgag

19

<210> 28

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 28

cccgagacg ctcaacatc

19

<210> 29

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 29

cagcgagtgg tcgatacctc c

21

<210> 30

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 30

gcggatccac catggcccaa gccc

24

<210> 31

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 31

ggggaattca cttcagcagg gagatgtcat cag

33

<210> 32

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> fluorogenic APP-based peptide MCA

<220>

<221> MOD_RES

<222> (10)..(10)

<223> AMIDATION

<400> 32

Ser Glu Val Asn Leu Asp Ala Glu Phe Lys
1 5 10